IN THE CLAIMS

Please amend the claims as follows:

1. (Currently Amended) A method of analyzing prokaryotic gene expression comprising:

removing ribosomal RNA from total RNA obtained from a prokaryotic cell to obtain a fraction of the total RNA enriched in mRNA;

adding a polyadenylation sequence at the 3' end of the isolated mRNA to obtain polyA-mRNA;

synthesizing a cDNA from the polyA-mRNA;

attaching a first adapter polynucleotide sequence at one end of the cDNA and a second adapter polynucleotide sequence at the other end of the cDNA to obtain an adapter-attached cDNA;

amplifying adapter-attached cDNA in a polymerization chain reaction (PCR) with a first primer which has an arbitrary dibasic sequence selected from A, T, G and C at the 3' end and has ~~having~~ a sequence complementary to a sequence of the first adapter and a second primer ~~having~~ which has an arbitrary dibasic sequence selected from A, T, G and C at the 3' end and has a sequence complementary to a sequence of the second adapter ;

isolating and recovering the amplified cDNA; and

analyzing prokaryotic gene expression with the recovered amplified cDNA.

2. (Previously Presented) The method according to Claim 1, wherein isolating the mRNA comprises:

hybridizing a first polynucleotide having a sequence complementary to at least a portion of 16S rRNA with the 16S rRNA, and simultaneously hybridizing a second

polynucleotide having a sequence complementary to a portion of 23S rRNA with the 23S rRNA;

wherein the third polynucleotide comprises a sequence complementary to the first polynucleotide at a site that is different from the site in which the first polynucleotide is complementary to the 16S rRNA in the first nucleotide thereby forming 16s rRNA hybrid molecules, and

a fourth polynucleotide which is coupled to a second tag substance wherein the fourth polynucleotide comprises a sequence complementary to the second polynucleotide at a site that is different from the site in which the second polynucleotide is complementary to the 23S rRNA thereby forming 23S rRNA hybrid molecules; and

removing the 16S rRNA and 23S rRNA hybrid molecules using the first and second tag substances from the whole RNA.

3. (Previously Presented) The method according to Claim 2, wherein

the first polynucleotide and the second polynucleotide are identical and comprise a sequence complementary to a common sequence present in both 16S rRNA and 23S rRNA,

the third polynucleotide and the fourth polynucleotide are identical, and

the first tag substance and the second tag substance are identical.

4. (Previously Presented) The method according to Claim 1, wherein

synthesizing a cDNA further comprises adding a tag substance ~~at~~ to the 5' end of the cDNA at the same time as the cDNA is synthesized; and

wherein after the cDNA is synthesized, the cDNA is cleaved with a type I restriction enzyme;

recovering the tagged cDNA with a high-affinity substance having high affinity to the tag substance;

wherein the first adapter comprises a sequence complementary to the sequence at the cleavage site of the type I restriction enzyme;

cleaving the cDNA attached to the first adapter with a type II restriction enzyme;

recovering the cDNA which does not have the tag substance; and

wherein the second adapter comprises a sequence complementary to the sequence at the cleavage site of the type II restriction enzyme.

5. (Previously Presented) The method according to Claim 1, wherein

isolating and recovering the amplified cDNA comprises subjecting the amplified cDNA to gel electrophoresis; and

recovering the amplified cDNA by cutting out a portion of the gel containing the cDNA-and recovering the cDNA from the gel.

6. (Previously Presented) The method according to Claim 5, wherein at least one of the first primer and the second primer are labeled with a marker substance, and wherein the marker substance is detectable in the gel.

7. (Previously Presented) The method according to Claim 4, wherein the tag substance and the high-affinity substance is any one of a combination of biotin and streptavidin, biotin and avidin, FIGT and FITI antibody, and DIG and anti-DIG.

8. (Previously Presented) The method according to Claim 1, which further comprises, after recovering the cDNA, ligating the recovered cDNA to a plasmid vector to form a recombinant plasmid; and

transforming an *Escherichia coli* cell with the recombinant plasmid.

9. (Previously Presented) The method according to Claim 8, which further comprises, after recovering the cDNA fragment and before ligating the recovered cDNA into a plasmid vector, amplifying the recovered cDNA with a third primer having a sequence complementary to the sequence of the first adapter and a fourth primer having a sequence complementary to the sequence of the second adapter.